

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/529,009
Source: PT/10
Date Processed by STIC: 4/1/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/529,009

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/529,009

DATE: 04/01/2005
TIME: 10:11:17

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\04012005\J529009.raw

2 <110> APPLICANT: JURIDICAL FOUNDATION THE CHEMO-SERO-THERAPEUTIC RESEARCH INSTITUTE
W--> 3 <120> TITLE OF INVENTION: Antibody against von Willebrand Factor cleaving protease and
the assay
W--> 4 method using the antibody thereof
W--> 5 <130> FILE REFERENCE: PH-1893-PCT
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/529,009
C--> 7 <141> CURRENT FILING DATE: 2005-03-24
7 <150> PRIOR APPLICATION NUMBER: JP 2002/279924
8 <151> PRIOR FILING DATE: 2002-09-25
10 <150> PRIOR APPLICATION NUMBER: JP 2002/377569
11 <151> PRIOR FILING DATE: 2002-12-26
E--> 13 <160> NUMBER OF SEQ ID NOS: ²⁰19-210>1

*see item 4 on
Err summary sheet*

**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES

(see p.5) 20 ← insert a hard return here

14 <211> LENGTH: 1427
15 <212> TYPE: PRT
16 <213> ORGANISM: Homo sapiens

OK 17 <400> SEQUENCE: 1 *see p.5.*
18 Met His Gln Arg His Pro Arg Ala Arg Cys Pro Pro Leu Cys Val
19 1 5 10 15
20 Ala Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro
21 20 25 30
22 Ser His Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala
23 35 40 45
24 Val Ser Ser Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro
25 50 55 60
26 Pro Ser Pro Gly Phe Gln Arg Gln Arg Gln Arg Gln Arg Ala
27 65 70 75
28 Ala Gly Gly Ile Leu His Leu Glu Leu Leu Val Ala Val Gly Pro
29 80 85 90
30 Asp Val Phe Gln Ala His Gln Glu Asp Thr Glu Arg Tyr Val Leu
31 95 100 105
32 Thr Asn Leu Asn Ile Gly Ala Glu Leu Leu Arg Asp Pro Ser Leu
33 110 115 120
34 Gly Ala Gln Phe Arg Val His Leu Val Lys Met Val Ile Leu Thr
35 125 130 135
36 Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala Asn Leu Thr Ser Ser
37 140 145 150
38 Leu Leu Ser Val Cys Gly Trp Ser Gln Thr Ile Asn Pro Glu Asp
39 155 160 165
40 Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu Tyr Ile Thr Arg

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41		170		175		180
42	Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val Arg Gly Val					
43		185		190		195
44	Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu Ile					
45		200		205		210
46	Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His Glu					
47		215		220		225
48	Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser					
49		230		235		240
50	Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala					
51		245		250		255
52	Pro Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu					
53		260		265		270
54	Leu Ser Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro					
55		275		280		285
56	Pro Arg Pro Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln					
57		290		295		300
58	Pro Gly Leu Tyr Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe					
59		305		310		315
60	Gly Pro Lys Ala Val Ala Cys Thr Phe Ala Arg Glu His Leu Asp					
61		320		325		330
62	Met Cys Gln Ala Leu Ser Cys His Thr Asp Pro Leu Asp Gln Ser					
63		335		340		345
64	Ser Cys Ser Arg Leu Leu Val Pro Leu Leu Asp Gly Thr Glu Cys					
65		350		355		360
66	Gly Val Glu Lys Trp Cys Ser Lys Gly Arg Cys Arg Ser Leu Val					
67		365		370		375
68	Glu Leu Thr Pro Ile Ala Ala Val His Gly Arg Trp Ser Ser Trp					
69		380		385		390
70	Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val					
71		395		400		405
72	Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly					
73		410		415		420
74	Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr					
75		425		430		435
76	Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln Gln Cys					
77		440		445		450
78	Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly Ala					
79		455		460		465
80	Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp					
81		470		475		480
82	Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile					
83		485		490		495
84	Met Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro					
85		500		505		510
86	Ser Gly Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly					
87		515		520		525
88	Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln					
89		530		535		540

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```

90 Val Trp Asp Arg Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys
91                               545                               550                               555
92 Ser Pro Arg Lys Gly Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr
93                               560                               565                               570
94 Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr Ile
95                               575                               580                               585
96 Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly
97                               590                               595                               600
98 Gly Arg Tyr Val Val Ala Gly Lys Met Ser Ile Ser Pro Asn Thr
99                               605                               610                               615
100 Thr Tyr Pro Ser Leu Leu Glu Asp Gly Arg Val Glu Tyr Arg Val
101                               620                               625                               630
102 Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile
103                               635                               640                               645
104 Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln Val Tyr Arg Arg
105                               650                               655                               660
106 Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp Ile Thr Phe
107                               665                               670                               675
108 Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp Ala Ala
109                               680                               685                               690
110 Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg Trp
111                               695                               700                               705
112 Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
113                               710                               715                               720
114 Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu
115                               725                               730                               735
116 Ala Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp
117                               740                               745                               750
118 Phe Gly Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg
119                               755                               760                               765
120 Pro Val Arg Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu
121                               770                               775                               780
122 Pro Pro Ala Arg Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala
123                               785                               790                               795
124 Leu Glu Thr Cys Asn Pro Gln Pro Cys Pro Ala Arg Trp Glu Val
125                               800                               805                               810
126 Ser Glu Pro Ser Ser Cys Thr Ser Ala Gly Gly Ala Gly Leu Ala
127                               815                               820                               825
128 Leu Glu Asn Glu Thr Cys Val Pro Gly Ala Asp Gly Leu Glu Ala
129                               830                               835                               840
130 Pro Val Thr Glu Gly Pro Gly Ser Val Asp Glu Lys Leu Pro Ala
131                               845                               850                               855
132 Pro Glu Pro Cys Val Gly Met Ser Cys Pro Pro Gly Trp Gly His
133                               860                               865                               870
134 Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala Pro Ser Pro Trp Gly
135                               875                               880                               885
136 Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val Trp Thr Pro Ala
137                               890                               895                               900
138 Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu Met Glu Leu

```

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139		905		910		915
140	Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val Gln Glu					
141		920		925		930
142	Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu Val					
143		935		940		945
144	Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala					
145		950		955		960
146	Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu					
147		965		970		975
148	Tyr Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu					
149		980		985		990
150	Leu Asp Thr Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu					
151		995		1000		1005
152	Ala Cys Ser Leu Glu Pro Cys Pro Pro Arg Trp Lys Val Met Ser					
153		1010		1015		1020
154	Leu Gly Pro Cys Ser Ala Ser Cys Gly Leu Gly Thr Ala Arg Arg					
155		1025		1030		1035
156	Ser Val Ala Cys Val Gln Leu Asp Gln Gly Gln Asp Val Glu Val					
157		1040		1045		1050
158	Asp Glu Ala Ala Cys Ala Ala Leu Val Arg Pro Glu Ala Ser Val					
159		1055		1060		1065
160	Pro Cys Leu Ile Ala Asp Cys Thr Tyr Arg Trp His Val Gly Thr					
161		1070		1075		1080
162	Trp Met Glu Cys Ser Val Ser Cys Gly Asp Gly Ile Gln Arg Arg					
163		1085		1090		1095
164	Arg Asp Thr Cys Leu Gly Pro Gln Ala Gln Ala Pro Val Pro Ala					
165		1100		1105		1110
166	Asp Phe Cys Gln His Leu Pro Lys Pro Val Thr Val Arg Gly Cys					
167		1115		1120		1125
168	Trp Ala Gly Pro Cys Val Gly Gln Gly Thr Pro Ser Leu Val Pro					
169		1130		1135		1140
170	His Glu Glu Ala Ala Ala Pro Gly Arg Thr Thr Ala Thr Pro Ala					
171		1145		1150		1155
172	Gly Ala Ser Leu Glu Trp Ser Gln Ala Arg Gly Leu Leu Phe Ser					
173		1160		1165		1170
174	Pro Ala Pro Gln Pro Arg Arg Leu Leu Pro Gly Pro Gln Glu Asn					
175		1175		1180		1185
176	Ser Val Gln Ser Ser Ala Cys Gly Arg Gln His Leu Glu Pro Thr					
177		1190		1195		1200
178	Gly Thr Ile Asp Met Arg Gly Pro Gly Gln Ala Asp Cys Ala Val					
179		1205		1210		1215
180	Ala Ile Gly Arg Pro Leu Gly Glu Val Val Thr Leu Arg Val Leu					
181		1220		1225		1230
182	Glu Ser Ser Leu Asn Cys Ser Ala Gly Asp Met Leu Leu Leu Trp					
183		1235		1240		1245
184	Gly Arg Leu Thr Trp Arg Lys Met Cys Arg Lys Leu Leu Asp Met					
185		1250		1255		1260
186	Thr Phe Ser Ser Lys Thr Asn Thr Leu Val Val Arg Gln Arg Cys					
187		1265		1270		1275

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188 Gly Arg Pro Gly Gly Gly Val Leu Leu Arg Tyr Gly Ser Gln Leu
 189 1280 1285 1290
 190 Ala Pro Glu Thr Phe Tyr Arg Glu Cys Asp Met Gln Leu Phe Gly
 191 1295 1300 1305
 192 Pro Trp Gly Glu Ile Val Ser Pro Ser Leu Ser Pro Ala Thr Ser
 193 1310 1315 1320
 194 Asn Ala Gly Gly Cys Arg Leu Phe Ile Asn Val Ala Pro His Ala
 195 1325 1330 1335
 196 Arg Ile Ala Ile His Ala Leu Ala Thr Asn Met Gly Ala Gly Thr
 197 1340 1345 1350
 198 Glu Gly Ala Asn Ala Ser Tyr Ile Leu Ile Arg Asp Thr His Ser
 199 1355 1360 1365
 200 Leu Arg Thr Thr Ala Phe His Gly Gln Gln Val Leu Tyr Trp Glu
 201 1370 1375 1380
 202 Ser Glu Ser Ser Gln Ala Glu Met Glu Phe Ser Glu Gly Phe Leu
 203 1385 1390 1395
 204 Lys Ala Gln Ala Ser Leu Arg Gly Gln Tyr Trp Thr Leu Gln Ser
 205 1400 1405 1410
 206 Trp Val Pro Glu Met Gln Asp Pro Gln Ser Trp Lys Gly Lys Glu
 207 1415 1420 1425
 208 Gly Thr
 209 ~~1427~~ delete - number the amino acids under every 5 amino acids

221 <210> SEQ ID NO: 3

222 <211> LENGTH: 18

223 <212> TYPE: PRT

224 <213> ORGANISM: Homo sapiens

OK-> 225 <400> SEQUENCE: 3

226 Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile Trp Gly Pro Leu

227 1 invalid amino 5 10 15

E--> 228 G1 Glu Asp acid designator

354 <210> SEQ ID NO: 20

355 <211> LENGTH: 8

E--> 356 <212> TYPE: ~~RPT~~ PRT

357 <213> ORGANISM: Artificial Sequence

WOK 358 <220> FEATURE:

359 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

W--> 360 <400> SEQUENCE: 20

361 Asp Tyr Lys Asp Asp Asp Asp Lys

362 1 5

363

(1/13) delete

VERIFICATION SUMMARY

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DATE: 04/01/2005

TIME: 10:11:18

Input Set : A:\PTO.FG.txt

Output Set: N:\CRF4\04012005\J529009.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
 L:5 M:283 W: Missing Blank Line separator, <130> field identifier
 L:7 M:270 C: Current Application Number differs, Replaced Current Application No
 L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:17 M:282 E: Numeric Field Identifier Missing, <210> is required.
 L:17 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:0 differs:1
 L:17 M:283 W: Missing Blank Line separator, <400> field identifier
 L:211 M:214 E: (33) Seq.# missing, SEQ ID NO:1
 L:215 M:283 W: Missing Blank Line separator, <400> field identifier
 L:225 M:283 W: Missing Blank Line separator, <400> field identifier
 L:228 M:333 E: Wrong sequence grouping, Amino acids not in groups!
 L:228 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
 L:228 M:252 E: No. of Seq. differs, <211> LENGTH:Input:18 Found:17 SEQ:3
 L:234 M:283 W: Missing Blank Line separator, <400> field identifier
 L:241 M:283 W: Missing Blank Line separator, <400> field identifier
 L:248 M:283 W: Missing Blank Line separator, <400> field identifier
 L:255 M:283 W: Missing Blank Line separator, <400> field identifier
 L:262 M:283 W: Missing Blank Line separator, <400> field identifier
 L:270 M:283 W: Missing Blank Line separator, <400> field identifier
 L:278 M:283 W: Missing Blank Line separator, <400> field identifier
 L:286 M:283 W: Missing Blank Line separator, <400> field identifier
 L:294 M:283 W: Missing Blank Line separator, <400> field identifier
 L:302 M:283 W: Missing Blank Line separator, <400> field identifier
 L:310 M:283 W: Missing Blank Line separator, <400> field identifier
 L:318 M:283 W: Missing Blank Line separator, <400> field identifier
 L:326 M:283 W: Missing Blank Line separator, <400> field identifier
 L:334 M:283 W: Missing Blank Line separator, <400> field identifier
 L:342 M:283 W: Missing Blank Line separator, <400> field identifier
 L:349 M:283 W: Missing Blank Line separator, <220> field identifier
 L:351 M:283 W: Missing Blank Line separator, <400> field identifier
 L:356 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
 L:358 M:283 W: Missing Blank Line separator, <220> field identifier
 L:360 M:283 W: Missing Blank Line separator, <400> field identifier
 L:13 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (19) Counted (20)